

Figure 1.

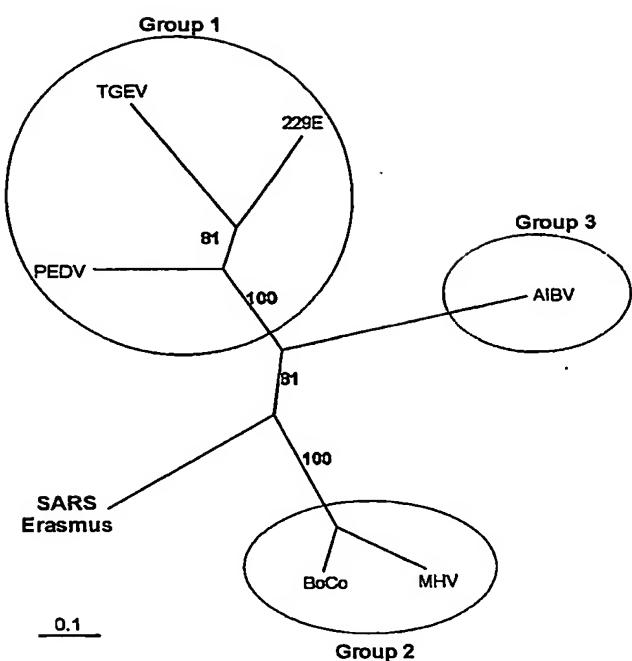


Figure 2 RNA sequences, implied polypeptides and alignment with one close relative

EMC-1

5 UUGUAACUGGUGGUUCUUGUACAACAGACUUUCUCAGGGUUGUCUAUUCUUUUGGCACUACUGGUUGAAAAAC
 UCAGGCCUAUCUUUGAUGGAUUGAGGCAGAAACUUAGUGCAGGAGUUGAAUUCUCAAGGAUGCUUGGGAGAU
 UCUCAAAUUCUCAUUACAGGUGUUUUGACAUCGUCAAGGGUAAAACAGGUUGCUUCAGAUAAACAUCAAG
 GAUUGUGUAAAUGCUUCAUUGAUGUUGUAAACAAGGCACUCUGAAAUGUGCAUGAUCAAGUCACUAUCGUG
 GCGCAAAGUUGCGAUACACUACUUAGGUGAAGCUUCAUCGUCAAAAGCAAGGGACUUUACCGUCAGUGUAU
 10 ACGUGGCAAGGAGCAGCUGCAACUACUCAUGCCUCUUAAGGCACCAAAAGAAGUAACCUUUCU
 UGAAGGUGAUUCACAUGACACAGUACUACCUCUGAGGAGGUUGUCUCAAGAACGGUGAA
 CUCGAAGCACUCGAGACGCCGUUGAUAGCUUCACAAUAGGAGCUCUACUGGUUGGCACACCAG
 UCUGUGUAAAUGGCCUCAUGCUCUUAGAGAUUAAGGACAAAGAACAAUACUGCGCAUUGUC
 UCCUGGUUUACUGGCUACAA AUGCUUUUCGUUAAAAGGGGUGGCACAAUUAAGGU
 15 GUAAACCUUUUGGAGAAGAUACUGUUJUGGAAGUUCAGGGUUACAAGAAUGUGAGAAUCAU
 UUGAGCUUGAUGAACGUGUUGACAAAGUGCUUAAUGAAAAGUGUCUCUGUCUACACUGUUGA
 AUCCGGUACCGAAGUUACUGAGUUUGCAUGUGUUGCAUGAGCAGAGGUGUUGUGAAGACUUUA
 CAACCAGUUUCUGAUC

20 *Translation*Nucleotides 7 to 870: Frame 1; 288 aa

LVVLYNRLLSGCLIFWALLVEKLRPIFEWIEAKLSAGVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCVKCFIDVV
 NKALEMCIDQVTIAGAKLRSINLGEVFIAQSKELYRQCIRGKEQLQLMPKAPKEVTFLEGDSHDTVLTSEEVVLKNGEL
 EALETPVDSFTNGAIVGTPVCVNGLMMLLEIKDKEQYCALSPGILLATNNVFRKGAPIKGVTFGEDTVWEVQGYKNVRITF
 ELDERVDKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLPQVSD

25

Alignment

RNA-directed RNA polymerase (orf1a) murine hepatitis virus
 Identities = 72/285 (25%), Positives = 118/285 (41%)

30 Query: 49 FWALLVEKLRPIFEWIEAKLSAGVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCV 228
 F AL V +R I EW + L+ + W + L+ G+F + G I + + + V
 Sbjct: 638 FKALGVAVVRKITEWFD--LAVDIAASAAGWLKYQ-LVNGLFAVANGVITFVQE-VPELV 693

35 Query: 229 KCFIDVVNKALEMCIDQVTIA---GAKLRSINLGEVFIAQSKELYRQCIRGKEQLQLMP 399
 K F+D ++ ID ++++ G + V+A SK +Y + K +MP
 Sbjct: 694 KNFVDKFKAFFKVLIDSMSVSILSGLTVVKTASNRVLAGSK-VYE--VVQKSL SAYVMP 750

Query: 400 LKAPKEVTFLEGDSHDTVLTSEEVVLKNGEL--EALETPVDSFTNGAIVGTPVCVNGLM 573
 + E T L G+ V + V + L + P SF IV L
 40 Sbjct: 751 VGC-SEATCLVGEIEPAVFEDDVVDVVKAPLTYQGCCPKPTSFEKICIVDK-----L 801

Query: 574 LEIKDKEQYCAL----SPGILLATNNVFRKGAPIKGVTFGEDT-VWEVQGYKNVRITF 735
 K +O+ + + G+L F G K V F + V ++ + ++ITF
 45 Sbjct: 802 YMAKCGDQFYPVVVDNDTGVLDQCWRFPACAG---KKVEFNDKPKVRKIPSTRKIKITF 857

Query: 736 ELDERVDKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLPQVSD 870
 LD D VL++ CS + V+ + E VV +AV TL P +
 Sbjct: 858 ALDATFDVSLSKACSEFEVDKDVTLDLDEVVLDAVESTLSPCKE 902

50 **EMC-14**

CAUCCAGCUUCUUAAGGCAGCAUAUGAAAAUUUCAAUUCACAGGACAUCUUACUUGCACCAUUGUUGUCAGCA
 GGCAUAUUUGGUGCUAAACCACUUUCAGCUUACAAGUGUGCGUGCGACGGUUCGUACACAGGUUUUAUUG
 CAGUCAAUGACAAAGCUCUUUAUGAGCAGGUUGUCAUGGAUUAUCUGUAACCUGAAGCCUAGAGGUGGAAGC
 ACCUAAAACAAGAGGAGGCCACCAACAGAAGAUUCCAACACAGGAGGAGAAUCUGUGUACAGAACGCCUGUC
 GAUGUGAAGCCAAAAAUUAAGGCCUGCAUUGAUGAGGUUACCACACUGGAAGAAACUAAGUUUCUACCA
 AUAAGGUUACUCUUGGUUGCUGUAUCAUAGGUUACCAUGAUUCUGAGAACAGCUUAGGUGAAGA
 UAUGUCUUUCUUGAGAAGGAUGCACCUCUACAGGUAGGUGUAUCACUAGUGGUGUAUCACUUGUGUU

Fig. 2 Cont.

GUAAUACCUCCAAAAGGCUGGUGGCACUACUGAGAUGCUCUCAAGAGCUUUGAAGAAAGUGCCAGUUGAUG
AGUAUAUAAACCACGUACCCUGGACAAGGAUGUGCUGGUUAACACUUGAGGAAGCUAGACUGCUCUUAAAGAA
AUGAAAUCUGCAUUUAUGUACUACCUUCAGAACCUAUGCUAAGGAAGAGAUUCUAGGAACUGUAUCC
UGGAAUUGAG

5

Translation

Nucleotides 5 to 739: Frame 2; 245 aa

10 IQLLKAAAYENFNSQDILLAPLLSAGIFGAKPLQLQSLQVCVQTVRQVYIAVNDKALYEQVVMMDYLDNLKPRVEAPKQEEPPN
TEDSKTEEKSVVQKPVDVKPKIKACIDEVTTLEETKFLETNKLLFADINGKLYHDSQNMLRGEDMSFLEKDAPYMVGDV
TSGDITCVVIPSKKAGGTTEMLSRALKKVPUDEYITTYPGQGCAGYTLEEAKTALKCKSAFYVLPSEAPNAKEEILGTV
WN

Alignment

15 replicase polyprotein lab Human coronavirus 229E

Identities = 48/202 (23%), Positives = 83/202 (41%), Gaps = 13/202 (6%)
Frame = +2

20 Query: 8 LLKAAAYENFNSQDILLAPLLSAGIFGAKPLQLQSLQVCVQTVRT---QVYIAVNDKALYEQV 178
L+KA N Q L P+LS G IFG K SL+V + T +V++ + + +
Sbjct: 1371 LIKAYNTINNEQGTPPLTPILSCGIFGIKLETSLEVLLDVCNTKEVKVFVYTDTEVCKVKD 1430

25 Query: 179 VMDYLDNLKPRVEAPKQEEPPNTEDSKTEEKSVVQKPVDVKPKIKACIDEVTTLEETKF 358
+ L N++ +VE PK E P V KP V K +++ ++
Sbjct: 1431 FVSGLVNVQ-KVEQPKIEPKP-----VSVIKVAPKPYRVDGKFSYFTEDLLCVADDKPI 1483

30 Query: 359 L--TNKLLLFA DINGKLYHDSQNMLRG--EDMSFLEKDAP-----YMGDVITSGDITC 508
+ T+ +L D L + +L +D + K P + +G V+ +
Sbjct: 1484 VLFTDSMLTLDRGLALDNALSGVL SAAIKDCVDINKAIPSGNLIKFDIGSVV---VYM 1539

Query: 509 VVIPSKKAGGTTEMLSRALKKV 574
V+PS+K + R +K+
Sbjct: 1540 CVVPSEKDKHLDNNVQRCTRKL 1561

35

EMC-2

UCGAGAUUUcAUcUUGACGGUGCAGGUUCUUUCACUUGACAAACUAAAGAGUCUCUUAUCCUGCGGGAGGUU
AAGACAUAAAAGUGUUCACAACUGUGGACAACACUAAUCUCCACACAGCUUGUGGUAUGUCUAUGACAU
40 AUGGACAGCAGUUUGGUCCAACAUACUUGGAUGGUGCUGAUGUUACAAAAAACCUCAUAGUAAAUCUGA
GGGUAGACUUUCUUUGUACUACCUAGUGAUGACACACUACGUAGUGAAGCUUUCGAGUACUACAUACUU
GAUGAGAGUUUCUUGGUAGGUACAUGUCUGCUUUAACCACACAAAGAAAUGGAAA

Translation

Nucleotide 2 to 349: Frame 2; 116 aa

45 RDFILTQVQLSLDKLKSLLSLREVKTIVFTTVDNTNLHTQLVDMMSMTYQQQFGPTYLDGADVTKIKPHVNHEGKTFVLP
SDDTLRSEAFYYHTLDESFLGRYMSALNHTKKW

50

Alignment

> Bovine Coronavirus RNA-Dependent RNA polymerase

55 Identities = 25/90 (27%), Positives = 44/90 (48%)
Frame = +2

Query: 80 IKVFTTVDNTNLHTQLVDMMSMTYQQQFGPTYLDGADVTKIKPHVNHEGKTFVLPSSDTL 259
+ + TVD N + V + ++G+ G + DG +VTK K +N++GK FF + +
Sbjct: 1565 VDILLTVDGVNFTNRFPVPGESFGKSLGNVFCGVNVTKHKCDINYKGKVFQFDNLSSE 1624

60

Query: 260 RSEAFYYHTLDESFLGRYMSALNHTKKW 349
+A D+ L Y + L + KW+

Sbjct: 1625 DLKAVRSSNFQDQKELLAYYNMLVNCWKQ 1654

65

Fig. 2 Cont.

EMC13:

CUGAAGAAAGUAGUGGAAAUCUACCAUACAGAAGGAAGCUAAGAGUGUGACGUGAAAACUACCGAAGUUGU
 AGGCAAUGUCAUACUUAAAACCAUCAGAAGGUAAAAGUAACACAAGAGUUAGGUCAUGAGGAUCUAUG
 5 GCUUCUAGUGGAAAACACAAGCAUACAUUAAGAAACCUAAGAGCUUUCACUAGCCUAGGUUUAAAAA
 CAAUUGGCCACUCUAGGUAUUGCUGCAUUAAAAGGUUAGGUUAGGUUAGGUUAGGUUAGGUU
 CUUAGGACAAGCAGCAUUACAACAUCAAAUUGCGCUAAGAGGUUAGCACAACGUGGUUAAACAAUUAUG
 10 CCUUAUGGUUUUACAUUAUGGUUCCAAUUGGUUACUUAAAAGUACCAAUUCUAGAAUAGAGCUUCAC
 UACCUACAACUAUUGCUAAAAAUAGGUUAGAGGUUAGGUUAGGUUAGGUUAGGUUAGGUU
 GAAGUCACCCAAAUUUCUAAAUGGUUACAAUCGUUAUGGUUACUUAUCUAAUUGGUUAGGUUAGGUU
 15 CUAAUCUGUGUAACUGCUGCUUUGGUUACUCUUAUCUAAUUGGUUAGGUUACUUGGUUAGGUUAGGUU
 GAGAAUUGUAUCUAAAUCGUUAACGUUACUACUACUAGGUUUCUGUGAAGGUUUCUUAUGGUUAGGUU
 UUUAGUGGUUAGACUCCCUGAUUCUAAUCAGCUCUUGAAACCAUUCAGGUGACGAUUCAUCGUACAAG
 CUAGACUUGACAUUUAGGUUCUGGCCUG

15 Translation

>~out: 3 to 833: Frame 3 277 aa
 EEVVNEPTIQKEVIECDVKTTEVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKPNELSALGLKTIATHGIAA
 INSVPWSKILAYVKPFLGQAAITTSNCAKRLAQRFVNMPYVFLLFQLCTFTKSTNSRIRASLPTTIAKNSVKSVA
 20 KLC LDAGINYVKSPKFSKLFITIAMWLLLSSLICSLICVTAAGVLLSNFGAPSYCNGVRELYLNSSNVTTMDFCEGSFPC
 LSGLDSLDSPALETIQVTISSYKLDLTLGLAA

Alignment

bovine coronavirus RNA-dependent RNA Polymerase
 Identities = 50/269 (18%),

25 Query: 57 KTTEVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKPNELSALGLKTIATH- 233
 K +V +VI+ +K + L D+ ++ ++ N+LS+A+ + TI
 Sbjct: 2046 KPFKVEDSVIVNDDTSEIKYVKSLSLIVDVYDMWLTGCRYVRTANDLSMAVNPTIRKFI 2105
 30 Query: 234 --GIAAINSVPSKI-LAYVKPFLGQAAITTSNCAKRLAQRFN--NYMPYVFLLF--- 389
 G+ + S+P + L +KP N K + ++ N++ ++F LLF
 Sbjct: 2106 KEGMTLV-SIPIDLNLREIKPVF-----NVVKAVRNKISACFNFIKWLFVLLFGWI 2156
 35 Query: 390 -----QLCTFTKSTNSRIRASLPTTIAKNSVKSVAKLCLDAGINYVKSPKFSKLFITIAMW 554
 +T S++ L KN+ + + G + + +W
 Sbjct: 2157 KISADNKVIYTTEVASKLTCKLVALAFKNAFLTFKWSVVARGACIIAT-----IFLLW 2209
 Query: 555 XXXXXXXXXXXXXXXVTAAGVLLSNFGAPSYCNGVRELYLNSSNVTTM----- 695
 G L P++ + + ++ ++ T+
 40 Sbjct: 2210 FNFIYANVIFSDFYLPKIGFL-----PTFVGKIAQWIKSTFSLVTICDLYSIQDVGFKN 2263
 Query: 696 DFCEGSFPCSCICLGLDSLDSPALETIQ 782
 +C GS C CL+G D LD+Y A++ +Q
 Sbjct: 2264 QYCNGSIAQCFCLAGFDMLDNYKAIDVVQ 2292

45 **EMC-3**
 GUGGUAGAUUGUUAGUACUUGUUAAAACUUAUGCUCAGGCCACAUUAUGUGCGUUCU
 UGCUGCAUAGUUUGUUAUCGUUAUGCCAGUACAUACAUUGUCAUCCAUGAUGGUUAC
 50 ACAAAUGAAAUCAUUGGUACAAAGCCAUCAGGAUGGUGUCACUCGUGACAUCAUUCUA
 CUGAUGAUUGUUUGCAAAACAUAGCUGGUUUGACGCAUGGUUAGCCAGCGUGGUGG
 UUCAUACAAAAAUGACAAAGCUGGCCUGUAGCUGCAGGAGCAUCAUUAACAGAGAGAUUGGU
 UCUACCUCGUGUUUUUAGUGCUGUUGGCAACAUUUGCACACACCUUCCAAACUCAUUGA
 GUAUAGUGAUUUUGCUACCUCU

55 Translation

Nucleotide 3-449; 149 aa
 GKIVSTCFKMLKATLLCVLAALVCYIVMPVHTLSIHGYTNEIIGYKAIQDGVRDIISTDDCFANKHAGFD
 60 AWFSQRGGSYKNDKSCPVVAIITREIGFIVPGLPGTVLRAINGDFLHFLPRVFSAVGNICYTPSKLIEYSDF
 ATS

Fig. 2. Cont.

Alignment

> Murine Hepatitis Virus RNA-Dependent RNA polymerase

5 Identities = 48/126 (38%),

Query: 78 YIVMPVHTLSIHGYTNEIIGYKAIQDGVTTRDIISTDDCFANKHAGFDAWFSQRGG--SY 251
+ +MP + + D +K I +GV RD+ TD CFANK FD W+ G Y

Sbjct: 2859 WALMPTYAVHKSDMQLPLYASFVVIDNGVLRDVSVTDAFCFANKFNQFDQWYESTFGLAYY 2918

10 Query: 252 KNDKSCPVVAAIITREIGFIVPGLPGTVLRAINGDFLHFLPRTVSAGVNICYTPSKLIEY 431
+N K+CPVV A+i ++IG + +P TVLR LHF+ F+ CYTP I Y

Sbjct: 2919 RNSKACPVVVAVIDQDIGTLFNVPTTVLR-YGFHVLFHAFATDSVQCYTPHMQIPY 2977

15 Query: 432 SDFATS 449
+F S

Sbjct: 2978 DNFYAS 2983

EMC-4

20 ACAGACAUCAUACUUUCUGCUGUUCUGCAGAGUGGUUUUAGGAAAUGGCAUUCCGUCAGGCAAAGUUGAA
GGGUGCAUGGUACAAGUAACCUGUGGAACUACACUCUAAUUGGAUGUGUGGUUGGAUGACACAGUAUACUGUC
CAAGACAUCAUUCUGCACAGCAGAAGACAUGCUCUAAUCCUACUAUGAAGAUCUGCUAUUCGCAAAUCCAA
CCAUGCUUUCUUGUUCAGGCUGGCAAUUGUUCACUUCGUGUUUAUUGGCCAUUCUACUAUGCAAAUUGCUGCUU
AGGCUUAAAGUUGAUACUUCUACCCUAAAGACACCCAAGUUAUUUUGUCCGUAUCCAAACCUGGUCAAACAU
UUUCAGUUCUAGCAUGCACAAUUGGUUCACCUACUGGUUUUACUGUGGCCAUGAGACCUAAUCAUACAU
UAAAGGUUCUUCUUAUUGGAUCAUGUGGUAGUGUUGGUUUUACAUUGAUUAUGAUUGCGUGUCUUUCUGC
UAAUAGCAUCAUAUUGGAGCUCUCCAACAGGAGUACACGCUGGUACUGACUAGAAGGUAAAUCUAUGGUCAU
UUGUUGACAGACAAACUGCACAGGCUGCAGGUACAGACACAACAUACAUAAAUGUUUUGGCAUGGCUGUA
UGCUGCUGUUAUCAUCAUAGGUGAU

30

Translation

Nucleotides 2 to 679: Frame 2; 226 aa

QTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTLNGLWLDDTVYCPRHVICTAEDMLNP NYEDLLIRKSNSFLVQAG

35 NVQLRIGHSMQNCLLRLKVDTSNPKTPKYKFVRIQPGQTFSVLACYNGSPGVYQCAMRPNHTIKGSFLNGSCGSVGFI
DYDCVSFCYMHMELPTGVHAGTDLEGKFYGPVFVDRQTAQAAGTDTTITLNVLAWLYAAVINGD

Alignment

RNA-directed RNA polymerase murine hepatitis virus

40 Identities = 122/222 (54%)

Query: 8 SITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTLNGLWLDDTVYCPRHVICTAEDMLNP 187
S+T++ LQSG KM P+ KVE C+V VT G TLNLWLDD VYCPRHVIC++ DM +P

45 Sbjct: 3326 SVTTSFQSGIVKVMVSPTSKVEPICIVSVTYGNMTLNGLWLDDKVCYCPHVICSSADMTP 3385

Query: 188 NYEDLLIRKSNSFLVQAGNVQLRIGHSMQNCLLRLKVDTSNPKTPKYKFVRIQPGQT 367
+Y +LL R ++ F V +G + L V+ + MQ C L L V NP TPKY F ++PG+TF

50 Sbjct: 3386 DYPNLLCRVTSSDFCVMGRMSLTVMWSYQMCGCQLVLTQLNPNTPKYSFGVVKPGETF 3445

Query: 368 SVLACYNGSPGVYQCAMRPNHTIKGSFLNGSCGSVGFNIDYDCVSFCYMHMELPTGVH 547
+VLA YNG P G + +R +HTIKGSFL GSCGSVG+ + D V F YM +EL TG H

Sbjct: 3446 TVLAAYNGRPQGAFHVTLSSTIKGSFLCGSCGSVGVLTDGSVRFVYMHQELSTGCH 3505

55 Query: 548 AGTDLEGKFYGPVFVDRQTAQAAGTDTTITLNVLAWLYAAVIN 673
GTD G FYGP+ D Q Q D T T+NV+AWLYAA+ N

Sbjct: 3506 TGTDFSGNFYGPYRDAQVVQLPVQDYTQTVNVVAWLYAAIFN 3547

EMC-5

60 Note that this sequence is not fully in frame.

AGUUGGAAAAGAUGGCAGAUCAGGCUAUGACCAAAUGUACAAACAGGCAAGAUCUGAGGA
CAAGAGGGCAAAAGUAACUAGUGCUAUGCAAACAAUUGCUCUUCACUAUGCUUAGGAAGCUU

65 GAACACUUGUGAUGGUACACCUUUAACAUAGCAUCUGCACUCUGCACUCUGGGAAAUCAGCAAGU
GUUGAUGCGGAUAGCAAGAUJGUCAACUJUAGUGAAAUAACAUUGGACAUCACCAAAU

UGGUUGGCCCUUAUUGUUACAGCUCUAAGAGGCCAACUCAGCUGUAAAACUACAGAAU
UGAACUGAGUCCAGUAGCACUACGACAGAUGGUCCUGUGCGGUGGUACCACACAAACAGCU

UGUACUGAUGACAAUGCACUUGCCUACUAAACAUUCGAAGGGAGGUAGGUUGUGCUGG

Fig. 2. Cont.

CAUUACUAUCAGACCACCAAGAACUCAAUGGGCUAGAUUCCUAAGAGUGAUGGUACAGG
 UACAAUUUACACAGAACUGGAACCACCUUGUAGGUUUGUACAGACACACCAAAAGGGCU
 AAAGUGAAAUCUJGUACUJUCAAGGCUAAAACAACCUAAAAGGUACAGAAGUaCCUGCCAAU
 5 CAAGUJGUAGCUGCUACAGUACGUUCAGGCUGGAAAUGCUGGUACAGAAGUaCCUGCCAAU
 ACUGUGCUUUCUUCUGUGCUUUGCAGUAGACCCUGCUAAAGCAUAUaAAGGAUUACCUA
 GCAAGUGGAGGACAACCAACCAACUGUGUGAAGAUGUUGUGUACACACACUGGUACAG
 GACAGGCCAAUUAACUGUAACACCAGAACGUACAUGGACCAAGAGGUCCUYUGGUGGUUC
 AUGUUGUCUGUAUUGUAGAUGCCACAUUGACCAUCCAAAUCUAAAGGAYUCUGUGACUUG
 10 AAAGGUAGUAGCUGUACGUACCUACCUACCUACUUGUGCUAAUGGUACCCAGUGGGUUU
 GAAACACAGUCUGUACCGUCUGCGGAUGUGGAAAGGUUAUGGUAGUAGUUGUGACCAACU
 CCGCGAACCCUUGAUGCAGUCUGCGGAUGCAUCAMCGUUUUUAAACGGGUUGCGGUGUAA
 GUGCAGCCCUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUCUACAGGGCUUU
 UGAUAUUUACAACGAAAAGUUGCUGGUUYUGCAAAGUUCUAAAAACUAA

15 *Translation 1*

Nucleotide 3-701 ; 233 aa

LEKMAQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRKLNDALNNIINNARDGCVPLNIIPLTAAKLMVV
 VPDYGYKNTCDGNTFTYASALWEIQQVVDADSKIVQLSEINMDNSPNLAWPLIVTALRANS
 20 VALRQMSCAAGTTQTAETDDNALAYNNNSKGGRFVLALLSDHQDLKWARFPKSDGTG
 PKGPVKVLYFIKA

Translation 2

FKRVCGVSA-ARLTPCGTGTSTDVVYRAFDIYNEKVAGXAKFLK

25 *Alignment 1 of translation 1 sequence*

RNA-Dependent RNA Polymerase: bovine coronavirus
 Identities = 181/413 (43%),

Query: 3 LEKMAQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRXXXXXXXXXXRDGCVPLN 182
 LE+MAD A+T MYR+AR DK++KV SA+QTMLF+M+RK GCVPLN
 Sbjct: 3985 LERMADLALTNYMKEARINDKKSKVVSALQTMFLSMVRKLDNQALNSILDNAVK
 GCVPLN 4044

Query: 183 IIPLTTAAKLMVVVPDYGYKNTCDGNTFTYASALWEIQQVVDADSKIVQLSEINMDNSP 362
 IP A L ++VPD Y D TYA +W+IQ + D+D QL+EI+ D +
 35 Sbjct: 4045 AIPSLAANTLTIIVPDKSYDQVVDNVYVTYAGNVWQIQTIQDGTNKQLNEIS
 DDCN- 4103

Query: 363 NLAWPLIVTALRAN--SAVKLQNNELSPVALRQMSCAAGTTQTAETDDNALAYNNNSKG 536
 WPL++ A R N SA LQNNEL P L+ +G QT T YNNNS G
 40 Sbjct: 4104 ---WPLVIIANRNEVSATVLQNNELMPAKLKTQVVNSGPDQTCTPTQ--CYNNNSNN 4158

Query: 537 RFVLLALLSDHQDLKWARFPKSDGTGTYTELEPPCRFTDTPKGPKVLYFIKA*TT*I 716
 + V A+LSD LK+ + K DG + EL+PPC+F KG K+KYLYF+K T
 Sbjct: 4159 KIVYAILSDVDSLKYTKILKDDG-NFVVLELDPPCKFTVQDVGLKIKYLYFVK
 GCNTLA 4217

Query: 717 EVWCWAV*LLQYVFRL-----EMLQKYLPIQLCFPSVLLQ*TLLKHDKYLASGGQPIT 878
 W V + RL E + LC SV + T L D++ GG PI
 Sbjct: 4218 R--GWVVGTISSTVRLQAGTATEYASNSSLCAFSDVPKKTYL---DFIQQQGTPIA 4271

Query: 879 NCVKMLCHTGTGQAITVTPEANMDQESXGGASCLYCRCHIDHPNPKGXCDLKGKYVQI 1058
 NCVKMLC H GTG AITV P+A +Q+S GGAS C+YCR ++HP+ G C L+GK+VQ+
 Sbjct: 4272 NCVKMLCDHAGTMAITVKPDAATTNQDSYGGASVCIYCRARVEHPVDGLCKLRGFVQV 4331

Query: 1059 PTTCANDPVGFTLRTNTVCTVCGMWKGYGCSCDQLREPLMQSADASXFLNGFAV 1217
 P DPV + L + VC VCG W+ CSC + +QS D + FLNGF V
 55 Sbjct: 4332 PVG-IKDPVSVLTHDVCQVCGFWRDGSCSCVS-TDTTVQSKDTN-FLNGFGV 4381

60 *Alignment 2 of translation 2 sequence*

RNA-directed RNA polymerase (ORF1B) [murine hepatitis virus]

Identities = 24/44 (54%),

Query: 1199 FKRVCGVSA-ARLTPCGTGTSTDVVYRAFDIYNEKVAGXAKFLK 1327
 FKRV G S ARL PC +G TDV RAFDI N AG + K
 65 Sbjct: 18 FKRVRGTSVNARLVP CASGLD TDVQLRAFDICNANRAGIGLYK 61

Fig. 2. Cont.

Translation 1

30 Nucleotides 3 to 818: Frame 3 272 aa (orf lab)
LQNYGENAVIPQGIMMVAKYTQLCQYLNTLTLAVPYNMRVIIHFGAGSDKGVAPGTAVLRQWLPTGTLLVDSDLNDFVSDA
DSTLIGDCACTVHTANKWDLIISDMYDPRTKHVTKENDSKEGFFTYLCGFIKQKLALGGSIAVKITEHSWNADLYKLMGHFS
WWTAFTVTVNNASSSEAFLIGANYLIGKPKEQIIDGYTMHANYIFWRNTNPQLSSYSLFDMSKFPLKLRGTAVMSLKENQIND
35 MIYSLLEKGRLIIRENNRVVVSSDILVNN

Translation 2

40 Nucleotide 828 to 3089: Frame 3 756 aa (S protein)
 MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSMRGVYYPDEIIFRSDTLYLTQDLFLPFYSNVTFHINTFGNPVI
 PFKDGIYFAATEKSNVVRGVWFGSTMNNKSQSIVIIINNSTNVVIRACNFELCDNPFFAVSKPMGTQTHMIFDNANFNTFE
 YISDAFSLDVSEKSGNFKHLREFVFKNKDGFLVYKGYQPIDVVRLPLSGFNTLKPFIKLPLGINITNFRAILTAFSPAQD
 IWGTSAAAYFVGYLKPPTFMLKYDENGTITDAVDCSQNPLAELKCSVSEI^{DKGIY}QTSNFRVVPSGDVVRFPNITNLCP
 45 FGEVFVNATKFPSPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCSNVYADSFVVVKGDDVRQIAPGQTGVIV
 ADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDI^SNVPFSPDGKPCTPPALNCYWP^LDYGFYT
 TGIGYQPYRVVVLSEELLNAPATVCGPLKSTD^LIKNQCVNFNGLTGTGV^LPSSKRFPQQFGRDVSDFTDSVRDPKT
 SEILDSPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIY^STGNNV^FQTQAGCLIGAEHVDTSYEC
 50 DIPIGAGICASYHTVSSLRSTSOKSIVAYTMSLGA^DSSIAYSNNTIA^IPTNFSISITTEVMPVSMAKTSVDCNMYICGDST
 ECANLLLQYGSFC^TQLNRALS^WYCC

Alignment 1 of translation 1

55 replicase [bovine coronavirus]
Identities = 183/271 (67%),

Query: 3 LQNYGENAVIPQGIMMNVAKYTQLCQYLNTLTLAVPYNMRVIHFGAGSDKGVAPGTAVLR 182
L NYG+ +P G MMNVAKYTQLCQYLNT TLAVP NMRV+H GAGS+KGVAPG+AVLR

60 Sbjct: 6822 LWNYGKPVTLPTGCMNNVAKYTQLCQYLNNTTLAVPVMRVLHLGAGSEKGVAPGSAVLR 6881

Query: 183 QWLPTGTLLVSDLNDFVSDADSTLIGDCATVHTANKWDLIISDMYDPRTKHVTKENDSK 362
QWLW GT+LVD+DL FVSD+ +T GDC T+ +WDLIISDMYDP TK++ +N SK
Shift: 6880 QWLPTGTLLVSDLNDFVSDADSTLIGDCATVHTANKWDLIISDMYDPRTKHVTKENDSK 362

CE Sbjct: 6882 QWLPAGTILVNDLYPFVSDSVATYFGDCITLPFDCQWDLIIISDMYDPITKNICEYNVSK 6941

Query: 363 EGFFTYLCGFIKQKLALGGSIAVKITEHWSWNADLYKLMGHSWWTAFTVNVNASSSEAFL 542
+GFETY+C I+ KLA+LGGS+A+KITE SWNA+I+YKLMG+F+I+WT F TN NASSSE FL

Fig. 2. Cont.

Sbjct: 6942 DGFFTYICHMIRDKLALGGSAIKITEFSWNAELYKLMGYFAFWTVFCTNANASSSEGFL 7001
 Query: 543 IGANYLGKPKEQIDGYTMHANYIFWRNTNPIQLSSYSLFDMSKFPLKLRGTAVMSLKENQ 722
 5 Sbjct: 7002 IGINYLGKEPKVEIDGNVMHANYLFWRNSTVWNNGAYSLFDMAKFPLKLAGTAVINLRADQ 7061
 Query: 723 INDMISSLLEKGRLIIRENRRVVVSSDILVN 815
 INDM+YSLLEKG+L++R+ N+ V D LVN
 Sbjct: 7062 INDMVYSLLEKGKLLVRDTNKEVFVGDSL VN 7092
 10 Alignment 2 (*Spike protein of coronavirus*)
 E2 glycoprotein precursor - murine hepatitis virus (strain JHM); contains spike glycoprotein
 15 Identities = 199/798 (24%), Positives = 314/798 (39%), Gaps = 48/798 (6%)
 Frame = +3
 Query: 828 MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSM-----RGVYYP-DEI 965
 +F+F+L L G D F +Q NY + +S RG YY D +
 20 Sbjct: 2 LFVFIPLLPSCLGYIGD---FCIQTVNYNGNNASAPSISTEAVDVSKGRGTYYVLDLV 57
 Query: 966 FRSDTLYLTQDLFLPF---YSNV--TCFHTINHTFGNP--VIPFKDGIVFAATE-KSNV 1118
 + + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N
 Sbjct: 58 YLNATLLLGT---YYPVDGSNYRNLAFTGTNTLSLTWFKPFFLSEFNDGIFAKVQNLKTNT 115
 25 Query: 1119 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXRACNFELCDNFFFAVSKPMGTQHT 1277
 G V GS N C + +C P+ KP
 Sbjct: 116 PTGATSYFPTIVIGSILFGNTSYTVVLEPYNNIIMASVCTYTICQLPY-TPCKP----- 167
 30 Query: 1278 MIFDNAFNCTFEYISDAFSLDVSEKSGNFKHREFVKFKNDGFPLYVY---KGYQPIDVVR 1448
 N + + DV K R F F +LY + +G
 Sbjct: 168 -----NTNGNRVIGFWHTDVKPPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218
 35 Query: 1449 DLPSGFNTLKPIFKLPLGINITNFRAILTAFPSAIDIWGTSAAYFVGYLKPTTFMLKYD 1628
 D PS L F + +G + T + + +P T A Y+V L ++ ++
 Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPICTPTAG--STLAPLYWVTPLLKRQYLFNFn 273
 Query: 1629 ENGTITDAVDCSQNPLAELKCSVKSFEIDKGIVQTSNFRVPGDVVR-FPNITNLCFG 1805
 E G IT AVDC+ + ++E+KC +S G+Y S + V P G V R PN+ + C
 40 Sbjct: 274 EKGVITSAVDCASSYISEIKCKTQSLLPSTGVYDLSGYTVQPVGVVVYRRVPNLPD-CKIE 332
 Query: 1806 EVFNATKFPSPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADS 1985
 E A PS WER+ NC + S L + C + A+K+ +CF +V D
 Sbjct: 333 EWLTAKSVPSPLNWERRTFQNCNFNLSSLLRYVQAESLSCNNIDASKVYGMCFGSVSDK 392
 45 Query: 1986 FVVKGDDVRQIAPGQTGVIADNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHG 2165
 F + + G + + NYK+ C L ++ + T NYN R+G
 Sbjct: 393 FAIPRSRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVT-INNYPSSWNRRYG 451
 50 Query: 2166 KLRPFERDISNVPFSPDGKPCPPALNCYWPLNDYGFYTTGIGYQPYRVVVLSELLNA 2345
 + +ND R + + LLN
 Sbjct: 452 -----FKVND-----RCQIFANILLNG 468
 55 Query: 2346 --PATVCGPKL---STDLIKNCVNFNFGLTGTGVLT-PSSKRFQPFQQFGRDVSDFD 2507
 T C L +T++ CV ++ G+TG GV + + +Q DV+ +
 Sbjct: 469 INSGTTCSTDQLPNTEVATGVCVRYDLYGITGQGVFKEVKADYYNSWQALLYDVNGNLN 528
 Query: 2508 SVRDPKTSEILDISPCSFGGSVITPGTNASSEAVAVLYQDVNCVDVSTAIHADQLTPAWR 2687
 RD T++ I C G VS + E A+LY++NC+ V T + + P
 60 Sbjct: 529 GFRDLTTNKTYTIRSCYSGRVSAAY--HKEAPEPALLYRNINC SYVFTNNISREENPL-- 584
 Query: 2688 IYSTGNNVFQTQAGCLIGAEH--VDTSYECDIPIGAGICASYHTVSLR---STSQK--S 2846
 N F + GC++ A++ + C++ +GAG+C Y R ST + +
 Sbjct: 585 -----NYFDSYLGCVVNADNRTDEALPNCNLRMGAGLCVDYSKSRRARRSVSTGYRLTT 638
 65 Query: 2847 IVAYTMSLGADESSIAASN-NTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECA 3023
 Y L DS + + IPTNF+I E + + K ++DC ++CGD+ C
 Sbjct: 639 FEPYMPMLVNDSVQSVGGLYEMQIPTNFTIGHHEIFIQIRAPKVTIDCAAFVCGDNAACR 698
 70 Query: 3024 NLLLQYGSFCTQLNRALS 3077

Fig. 2. Cont.

L++YGSFC +N L+
Sbjct: 699 QQLVEYGSFCDNVNAILN 716

RDG1 seq

5 UUCAAAGCcUUCAAACNUAUGUAACACAACAAUCAGGGMUGcUGAAAUCHCGSCUUCUGCUAAUCUUGC
UGCUACUAAAUGUGUGAGUGGUUCUUGGACAAUCAAAAGAGUUGACUUUUGUGGAAAGGGCUACCACCUU
AUGGUCCUCCCAACAGCAGCCCCGCAUGGUGUUGUCUACAUAGUCAUGUACGUAUGUGCCAUCCCAGGAGAGGA
ACUUCACACAGCGCCAGCAUUAUGUCAUGAAGGCAAAGCAUACUUCUCCUGUGAAGGUGUUGUUGUUGUUA
UGGCACUUCUUGGUUUAUUAACAGAGGAACUUCUUCUCCACAAAUAUUAACUACAGACAAUACAUUUGUC
UCAGGAAAUGUGUGAUGUGGUUAUUGGCAUCAUUAACACAGUAAAUGAUCCUCUGCAACCUGAGCUUGAC
CAAUCAAGAAGAGCUGGACAAGUACUCAAAAUAUACAUACUACACCAGAUGUUGAUUUGGCGACAUUUCAGG
CAUUAACGCUUCUGUCGUCAACAUCAAAAAGAAAUGACCGCCUCAUGAGGUUCGUAAAUAUUAUGAA
UCACUCUCAUUGACCUUCAAGAAUUGGGAAAAUAUGAGCAAUAUUAAGUGGCCCUGGUACGUCUGGGU

15 Translation 1

Nucleotides 3 to 650: Frame 3; 216 aa
QSLQXYVTQQLIRXAEIXXSANLAATKMSECVLGQSKRVDFCGKGYHLMSPQAAPHGVVFLHVTYVPSQERNFTTAPAI
HEGKAYFPREGVFVFNNGTSWFTQRNFFSPQIITTDNTFVSGNCVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPD
20 VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVW

Translation 2

Nucleotides 37 to 339: Frame 1; 101 aa
SGXLKXXLLLILLLLKLSVFLDNQKELTFVERATTLCPSHKQPRMVLSYMSRMCHPRRGTPQRQQFVMKAKHTSLVKV
25 FLCLMALLGLLHRGTSFLHK

Translation 3

Nucleotides 343 to 576: Frame 1; 78 aa
LLQTIHLSQEIVMSLLASLTQFMILCNLSLTHSKKSWTSTSIIHHQMLILATFQALTLSSTFKKKLTASMRSILKI

30 Alignment of translation 1

S glycoprotein [murine hepatitis virus]
Length = 1376

35 Identities = 86/218 (39%), Positives = 129/218 (59%), Gaps = 3/218 (1%)
Frame = +3

Query: 6 SLQTYVTQQLIRXAEIXXSANLAATKMSECVLGQSKRVDFCGKGYHLMSPQAAPHGVVF 185
+L Y+++QL I SA A K++ECV Q+ R++FCG G H++S Q AP+G+ F
40 Sbjct: 1105 ALNAYISKQLSDSTLIKFSAAQAIKVNNECVKSQTTRINF CGNGNHILSLVQNAPYGLYF 1164

Query: 186 LHVTYVPSQERNFTTAPAIChEG-KAYFPREGVFVFNNGTSWFTQRNFFSPQIITTDNTF 362
+H +YVP+ +P +C G + P+ G FV + W T +++ P+ IT N+
Sbjct: 1165 IHFSYVPTSFTTANVSPGLCISGDRLAPKAGYFVQDDGEWKFTGSSYYPEPITDKNSV 1224

45 Query: 363 VSGNCVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDV DLDISGINASVVNI 536
V +C V + + P L FKEELDK+FKN TS PD+ L D +N + +
Sbjct: 1225 VMSSCSVNYTKAPEVLLNSSIPNLPDFKEELDKWFKNQTSIAPDSL-DFEKLNTFLDL 1283

50 Query: 537 QKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVW 650
E++R+ E K LNEs I+L+E+G YE Y+KWPWYVW
Sbjct: 1284 SDEMNRQEAIKKLNESYINLKEVGTYEMYVKWPWYVW 1321

55 EMC-8

AGGCCAAAACAGCGCCGACCCCCAAGGUUUACCCAAGGUUUACUACUGCGUUGGUUCACAGCUCUCACUCAGCAUG
GCAAGGAGGAACUAGAUUCCUCGAGGCCAGGGCGUCCAAUCAACACCAAUAGUGGUCCAGAUGACCAAAU
UGGUACUACCGAAGAGCUACCCGACGAGUUCGUGGUGGUGACGGCAAAAGAAAGAGCUCAGCCCCAGAUGG
UACUUCUAAUACCUAGGAACUGGCCAGAACGUUCACUUCUCCUACGGCGCUACAAAGAAGGCAUCGUUAUGGG
60 UUGCAACUGAGGGAGCCUUGAAUACACCCAAAGACCACAUUGGCACCCGCAAUCCUAAACAAUGUUGCC

Translation

Nucleotides 1 to 363: Frame 1; 121 aa
RPKQRPFQGLPNNTASWFTALTQHGKEELRFPRGQGVINTNSGPDDQIGYYRRATRRVRGGDGKMKELS PRWYFY LGTG
65 PEASLPYGANKEGIVVWATEGALNTPKDHIGHTRNPNNXA

Fig. 2. Cont.

Alignment

nucleocapsid protein - bovine coronavirus (strain Mebus)

5 Identities = 55/129 (42%),

Query: 1 RPKQRRPQGLPNNTA-----SWFTALTQHGK-EELRFPRGQGVINTNSGPDDQIGYYRR 162
+PKQ LP+ SWF+ +TQ K +E F GQGVPI + GY+ R

Sbjct: 44 QPKQTATSQLPSPGGNVVPPYSWFSGITQFQKGKEFEFAEGQGVPIAPGVATEAKGYWYR 103

10 Query: 163 ATRR-VRGGDGKMKELS PRWYFYYLGTGPEASLPYGANKEIVVVATEGA-LNTPKDHIGH 336
RR + DG ++L PRWYFYYLGTGP A YG + +G+ WVA+ A +NTP D I

Sbjct: 104 HNRRSFKTADGNQRQLLPRWYFYYLGTGPHAKDQYGTIDGVFWVASNQADVNTPAD-IL 162

15 Query: 337 TRNPNNNXA 363
R+P+++ A

Sbjct: 163 DRDPSSDEA 171

EMC-11: unknown sequence

20 UUGCAUACCGCAAUGUUUCUUCGUAGAACGGUAUAAGGGAGCCGGUGGUCAUAGCUGUGCAUGAUCUA

AAGCUUAUGACUUAGGUGACGAGCUUGGCACUGAUCCAUUGAAGAUUAUGAACAAAACUGGAACACUAAGC

AUGGCAGUGGUGCACUCCGUGAACUCACUGUGAGCUCAUUGAACAAUGGAGGUGCAGUCACUCGCUAUGUCGACAACAA

UUUCUGUGGCCAGAUGGGUACCCUCUUGAUUGCAUAAAGAUUUUCUGCAGCGCGGGCAAGUCAAUGUGC

ACUCUUCCGAACAAACUUGAUUACAUUGAGUCGAGUCCAGAGAGGUGUCUACUGCUGCCGUGACCAUGAGCAUGAAA

25 UUGCCUgGGUUCACUGAGCGCUCUGAUAAAGAGCUACGAGCACAGACACCCUUCAAGAAGAGGUGCCAAGA

AAaUUGACACUUCAAAAGGGAAUGCCCCAAAGCUUGUGUUUCCUUAACUAAAAGUCAAAGUCAAUCAA

CCACGUGUUGAAAAGAAAAAGACUGAGGGUUUCAUGGGCGUUAACGCUCUGUGUACCCUGUUGCAUCUCCAC

AGGAGUGUAACAAUAGCACUUGUCUACCUUAGAUGAAAUGUAUCAUUGCGAUGAAGCUUCAUGGCAGACGUG

CGACUUUCUGAAAGCCACUUGUGAACAUUGUGGCACUGAAAAUUUAGUUAUUGAAGGACCUAGUACAUGUGGG

30 UACCUACCUACUAUAGCUGUAGUGAAAUGCCAUGGUCCUGCCUGUCAAGACCCAGAGAUUUGGACCUGAGCAUA

GUGUUGCAGAUUAUCACAACCACUCAAACAUUGAAACUCGACUCCGCAAGGGAGGUAGGACUAGAUGUUUUGG

AGGCUGUGUUGUUGCCUAUGUUGGCUGCUUAUAAAAGCGUGCCUACUGGGUUCUGUGCUAGUGCUGUAUAU

GGCUCAGGCCAUACUGGCAUACUGGUGACAAUGUGGAGACCUUGAUGAGGAUCUUGAGAUACUGAGUC

GUGAACGUGUUUACAUUAACAUUGUUGGCAGUUUCAUUUGAAUGAAGAGGUUGCCAUCAYUUUGGCAUCYUU

35 CUCUGCUUCUACAAUGGCCUUUUAUGACACUUAUAAAGAGUCUUGAUUACAAGUCUUUCAAAACCAUUGUUGAG

UCCUGCGGUACAUUAAGUUAACCAAGGGAAAGCCCGUAAAAGGUGCUUGGAACAUUGGACAACAGAGAUCAG

UUUUACACACCACUGUGGGUUUCCUCACAGGCUGCUGGUUAUCAGAUCAUUUUUGCGCGCACACUUGA

UGCAGCAAACACCUUCCUGAUUUGCAAAGAGCAGCUGUCACCAUUGAUGGUUUUCUGAACAGUCA

UUACGUCUUGUGCAGCAGCCAUUGGUUAUACUUCAGACCUGCUCACCAACAGUGUCAUUAUUAUGGCAUAUGUAA

40 CUUGGUGGUCAUUGUACACAGACU

Translation of putative open reading frames

45 >~out: 78 to 1: Frame -2 26 aa

DFRSCHSYDHRLPYRYEEHCGMQ
>~out: 59 to 379: Frame 2 107 aa

LWHDILKSYDLGDELGTDPIEDYEQNWNTKHSGALRELTRELNGGAVTRYVDNNFCGPDGYPLDCIKDFLARAGKSMCTLSEQLDYIESKRGVYCCRDEHEIAWVH

50 >~out: 283 to 89: Frame -1 65 aa

LARACEKIFDAIKRVPIMATEIVVDIASDCTSIELTSEFTECTTAMLSPVPLFIIFNGISAKLVT

>~out: 90 to 614: Frame 3 175 aa

VTSLALIPLKIMNKGTLSMAVVHSVNSLVSSMEVQSLAMTTISVAQMGTILLIASKIFSHARASQCALFPNNLITSSRE

55 VSTAAVTMSMKLPGFTERSDKSYEHQTPFEIKSAKKIDTFKRGMPQSCLFLTQKSFSFNHLKRKRLRVSWGYYALCTLLHLHRSVTICTCLP

>~out: 204 to 124: Frame -2 27 aa

RVTAPPLSSRVSSRSAPLPCLVFQFCS

>~out: 312 to 208: Frame -2 35 aa

SSCSERVHIDLPARARKSLMQSRGYFSGPQKLLST

60 >~out: 485 to 258: Frame -3 76 aa

EETQALGHSPFESVNFLGTLNFEGLVLVALIRALSEPRQFHAGHGSSRHLSTRCNQVVRKECTLTCPRVRENLL

>~out: 397 to 287: Frame -1 37 aa

LLSERSVNPGNFMLMVTAAVDTSLRLDVJKLFGKSAH

65 >~out: 364 to 486: Frame 1 41 aa

NCLGSLSALTRATSTRHPSKLRLVPRKLTLSKGECPKACVSS

>~out: 490 to 401: Frame -1 30 aa

VKRKHKLWGIPLLKVSIFLALLISKGVWCSS

>~out: 446 to 1483: Frame 2 346 aa

Fig. 2. Cont.

HFQKGNAPKLVFPFLNSKVVKVIQPRVEKKTEGFMGRIRSVPVASPQECCNNMHLSLMCKNCDEASWQTCDFLKATCEHC
 GTENLVIEGPSTCGYLPTNAVVKMPCPACQDPEIGPEHHSVADYHNHSNIETRLRKGRTRCFGGCVFAYVGCVNKRAYWVP
 RASADIGSGHTGITGDNVETLNEDLLEILSRRERVNINIVGDFHLNEEVAIXLAXFSASTSAFIDTIKSFTKIVE
 GNYKVTKGKPVKGAWNIGQQRSLTPLCGFPSQAAGVIRSIFARTLDAANHSIPDLQRAVTILDGISEQSLRLVDAMVY
 5 SDLLTNSVIIMAYVTGGLVQQT
 >~out: 643 to 494: Frame -1 50 aa
 SFIAMITFHGRQVHVITLLWRCNRVHRAYTPHETLSLFLFNTWLNDFDF
 >~out: 627 to 511: Frame -2 39 aa
 LHFIKVDKCILLHSCGDATGYTERIRPMKPSVFFFSTRG
 10 LNFQCHNVHKWLSESRTSAMKLHRNDYISSR
 >~out: 774 to 631: Frame -2 48 aa
 QAGHGIFTTALVGRYPHVLGPSITKFSVPQCSQVAFRKSHVCHEASSQ
 >~out: 826 to 737: Frame -1 30 aa
 15 VVIIICNTMLRSNLWVLTGRTWHFHYSISR
 >~out: 863 to 744: Frame -3 40 aa
 SYLPCGVEFQCLSGCDNLQHYAQVQSQLGLDRQDMAFSLQH
 >~out: 756 to 992: Frame 3 79 aa
 20 KCHVLPVKTQRLLSIVLQIITTTQTLKLDSSAREVGLDVLEAVCLPMLAAIISVPTGFLVLVLILAQAILALLVTMWRP
 >~out: 952 to 830: Frame -1 41 aa
 ANISTSTRNPVGTLLIAANIGKHTASKTSSPTSLAESSFNV
 >~out: 1056 to 922: Frame -2 45 aa
 KSPTMLMLTRSRLSISRRSSFKVSTLSPVMPVWPEPISALARGTQ
 >~out: 1237 to 956: Frame -1 94 aa
 25 SLLSNVPSTFYGLSLGNFIVTAGLNNGFERLVIKTLYSVNKGTCRSREXCQXDGNLFIQMKIANNVNVNTFTTQYLKEILI
 QGLHIVTSNASMA
 >~out: 1140 to 1060: Frame -2 27 aa
 SRLFIVSIKALVEAEXDAKXMATSSFK
 >~out: 1131 to 1205: Frame 3 25 aa
 30 RVLITSLSKPLLSPAVTIKLPRESP
 >~out: 1410 to 1183: Frame -2 76 aa
 TMASTRRRNDCSEIPSSMVTAALCKSGIEWFAASSVRAKIDLITPAACEGKPHSGVKTDLCCPMFQAPFTGFPLVTL
 >~out: 1186 to 1311: Frame 1 42 aa
 SYQGKARKRCLEHWTTTEISFNTTVWFSLTGCWCYQINFCAHT
 35 >~out: 1283 to 1191: Frame -3 31 aa
 HQQPVRENHTVVVLKLISVVCQSKHLLRAFPW
 >~out: 1248 to 1457: Frame 3 70 aa
 HHCVVFPHRLLVLSQFLRAHLMQQTTQFLIKEQLSPYLMVFLNSHYVLSTPWFILOTCSPTVSLLWHM
 >~out: 1381 to 1482: Frame 1 34 aa
 40 TVITSCRRHGLYFRPAHQCHYYGICNWWSCTTD

EMC12: unknown sequence .

UGCUGCUCAUGCUGAACAGAAAAUUAUGCCUAUAUGCAUGGAUGUUAGAGCCA
 AAUGGCAACCAUCCAACGUAGUAAGUAAAAGGAAUAAAUCAGAGGGCAUCGUUGACAU
 45 GGUGUCCGAUUCUUCUUUAUACUAGUAAAAGAGGCCUGUAGCUUCUAUUAAUCGAAGCUGA
 ACUCUCUAAAUGAGCCGCUUGUCACAAUGCCAAUUGGUUAUGUGACACAUGGUUUUAUCU
 UGAAGAGGGCUGCGCUGUAUGCGUUCUCUAAAAGCUCCUGCCGUAGUGUCAGUAUCAUCA
 CCAGAUGCUGUUACUACAUAAAUGGAUACCUCACUUCGUCAUCAAAGACAUCUGAGGAGC
 ACUUJUGUAGAACAGUUUCUJUGGCUGGCUCUJACAGAGAUJUGGUCCUAUUCAGGACAGCG
 50 UACAGAGUUAGGUGUJUGAA

Translation of putative open reading frames

>~out: 3 to 446: Frame 3 148 aa
 LAHAETRKLMPICMDVRAIMATIQRKYKGKIKIQEGIVDYGVRFFYTSKEPVASIITKLNSLNEPLVTMPIGYVTHGFNL
 55 EEAARCMRSLKAPAVVSVSSPDAVTTNGYLTSKTSSEEHFVETVSLAGSYRDWSYSQRTTELGV
 >~out: 100 to 11: Frame -2 30 aa
 ILIPLYLRWMVAIMALTSMHIGINFLVSSA
 >~out: 188 to 33: Frame -1 52 aa
 RVQLRNNRSYRLFTSIKEESDTIVNDALLNFNSFILTDGCHYGSNIHAYRH
 60 >~out: 64 to 159: Frame 1 32 aa
 WQPSNVSISKELKFKRASLTMVSDSSFILVKSL
 >~out: 220 to 143: Frame -2 26 aa
 PIGIVTSGSFREFSFVIIIEATGSLLV
 >~out: 293 to 192: Frame -1 34 aa
 65 HYGRSFKRHTTARSLSFKIKTMCHITNWHDCKRLI
 >~out: 397 to 224: Frame -2 58 aa
 EPAKETVSTKCSSDVFDDEVRYPLYVVTASGDDTDTAGALRERIQRASSRLKPCVT
 >~out: 229 to 288: Frame 1 20 aa

Fig. 2. Cont.

HMLVLLKRLRAVCVLLKLLP
>-out: 292 to 372: Frame 1 27 aa
CQYHHQMLLHIMDTSLRHQHLRSTL
>-out: 444 to 340: Frame -3 35 aa
5 QHLTLYAVLNRTNLCKSQPKKLFLQSAPQMSLMTK
>-out: 416 to 351: Frame -1 22 aa
IGPISVRASQRNCFYKVLLRCL
>-out: 365 to 445: Frame 2 27 aa
10 GALCRNSFFGWLLQRLVLFRAYRVRC
>-out: 376 to 435: Frame 1 20 aa
KQFLWLALTEIGPIQDSVQS

Figure 3.

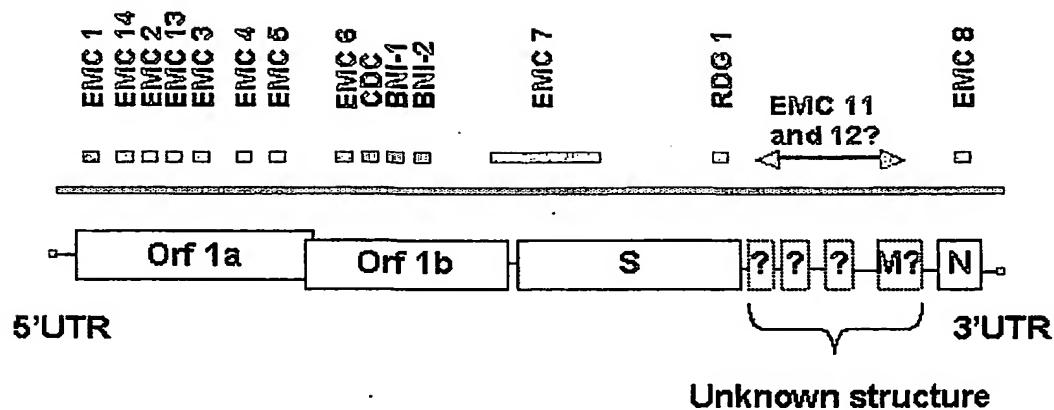


Figure 4.

Comparison of N-termini of the S proteins of the group 2 coronaviruses

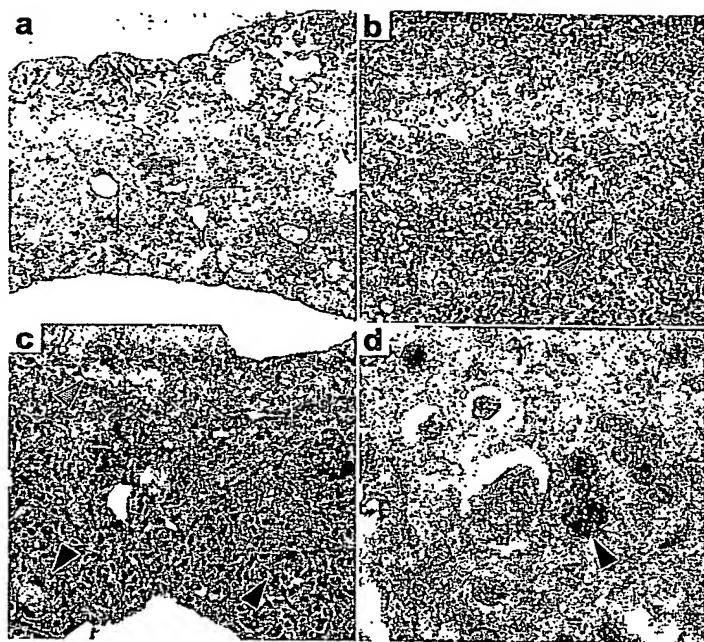
5

HCV OC43	MFLILLISLPTAFAVIGDL- KCTTVSINDID
MHV A59	MLFVFILFLPSCLGYIGDF- RCIQLVNSNGA
BCV	MFLILLISLPMAFAVIGDL- KCTTVSINDVD
SARS	MF-I FLLFL-TLTSG-SDLDRCTTFDDVQAP

10

Figure 5.



Figure 6.

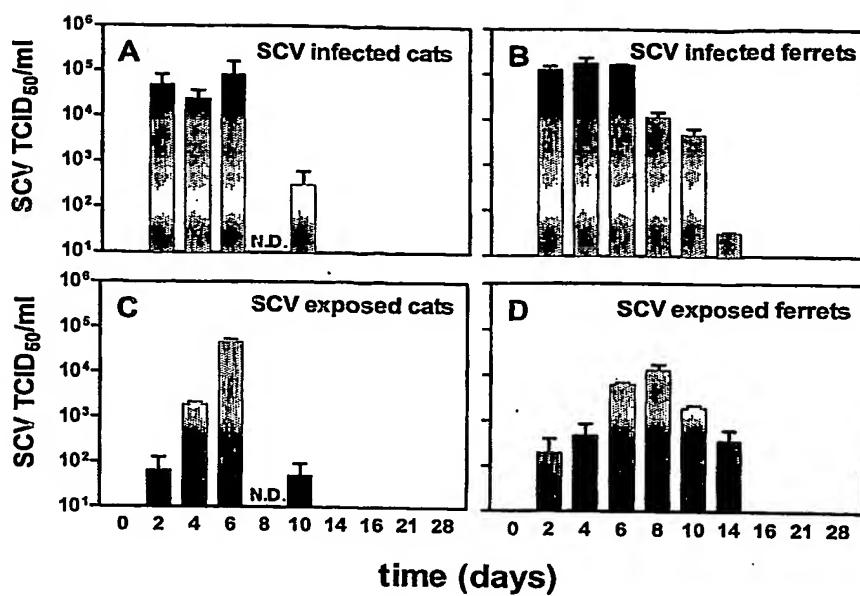


Figure 7.

Figure 8 Detection of SCV in postmortem tissues of experimentally SCV infected cats and ferrets

Tissue	Cats				Ferrets			
	1	2	3	4	1	2	3†	4
Trachea	+/	+/	+/	+	+/	+/	+/	+/
Lung	+*	+	+	+	+	+	+	+
Tracheo-bronchial lymph node	-/-	+/-	+/	-/-	+/-	+/-	+/-	+/-
Duodenum	-/-	-/-	-/-	+/	-/-	+/-	-/-	-/-
Jejunum	-/+	-/-	-/-	+	-/-	+/-	-/-	-/-
Ileum	-/-	+/-	-/-	-/-	+/-	+/-	-/-	-/-
Mesenteric lymph node	-/+	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Kidney	-/-	+/-	-/-	-/-	-/-	-/-	-/-	-/-
Urinary bladder	-/+	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Peripheral blood mononuclear cells	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-

* virus isolation/real time PCR results are depicted at day 4 p.i.

† died during the experiment.

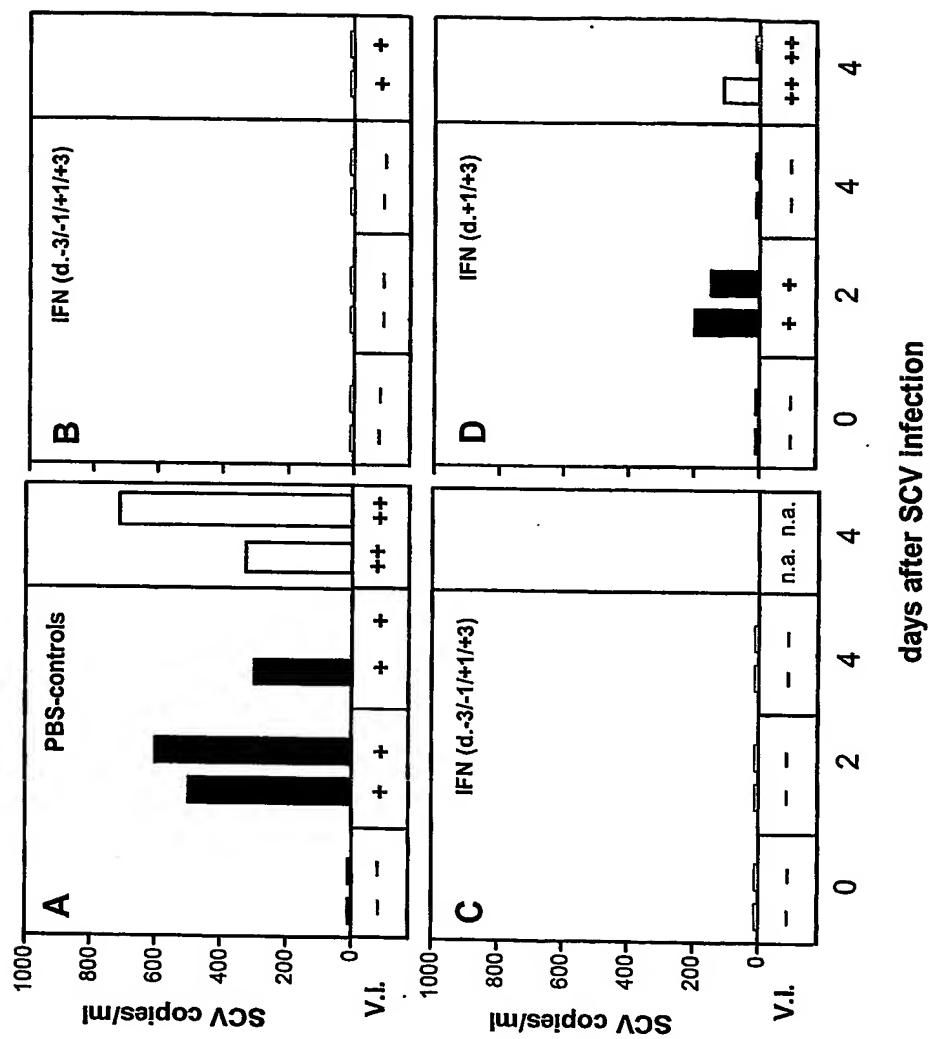


Figure 9

Figure 10

				cggatctttt
1	atattagggtt	tttacccatt	cagaaaaaagc	caaccaaacct
61	ctctaaacga	actttaaaat	ctgtgttagct	gtcgctcgcc
121	gcagttataaa	cataataaa	ttttactgtc	gttgacaaga
181	tctgcagact	gtttacgggt	tcgtcccggt	tgcagtctgat
241	gtccgggtgt	gaccggaaagg	taagatggag	agcccttgtc
301	cacgtcaac	tcagtttgcc	tgtcccttcag	gttagagacg
361	gactctgtgg	aaggccct	atcgaggca	cgtgaacacc
421	ctagtagagc	tggaaaaagg	cgtctggcc	cagcttgaac
481	cgttctgtatg	ccttaagcac	caatcacggc	cacaaggctg
541	gacggcattc	atgtacggctg	tagcggtata	acaactgggg
601	gaaacccaa	ttgcataccg	caatgtctt	cttcgttaaga
661	ggtcatagtct	atggcatcg	tctaaggctt	tatgacttag
721	ccccatggaaag	attatgaaca	aaactgtaaac	actaaaggat
781	ctcactctgt	agctcaatgg	agggtgcagtc	actcgctat
841	ccagatgggt	accctcttga	ttgcatacaa	gattttctcg
901	ttgcactttt	cgaacaact	tgattacatc	gagttcaaga
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Fig. 10. Cont

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Fig. 10. Cont.

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Fig. 10. Cont.

Fig. 10. Cont.

Fig 10. Cont.

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Fig 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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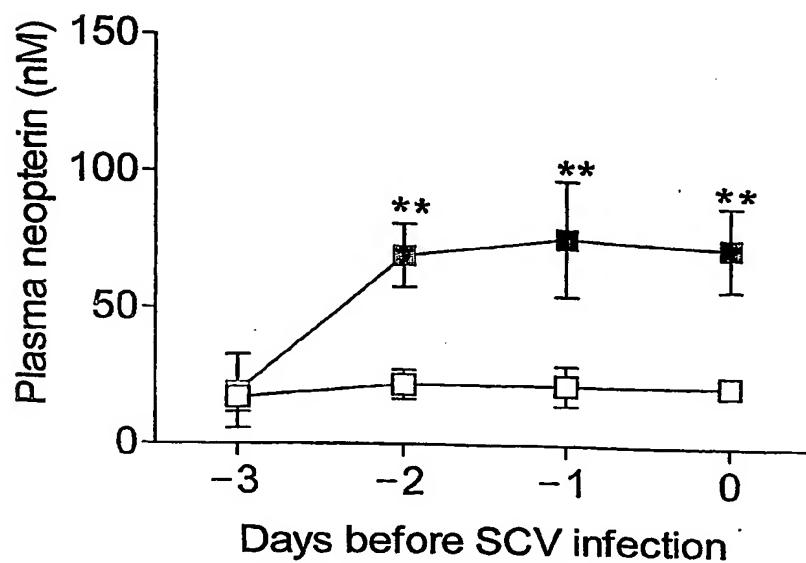
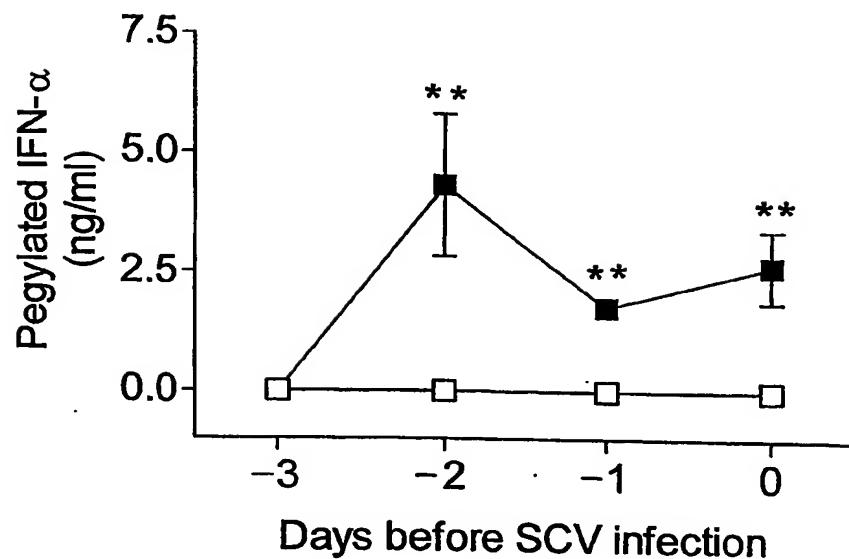
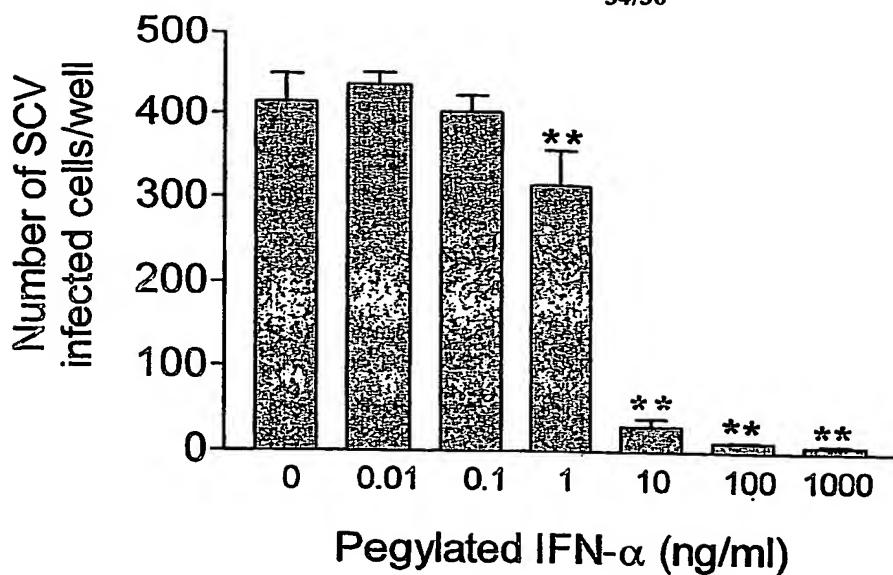
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Fig. 10. Cont.

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Fig. 10. Cont.

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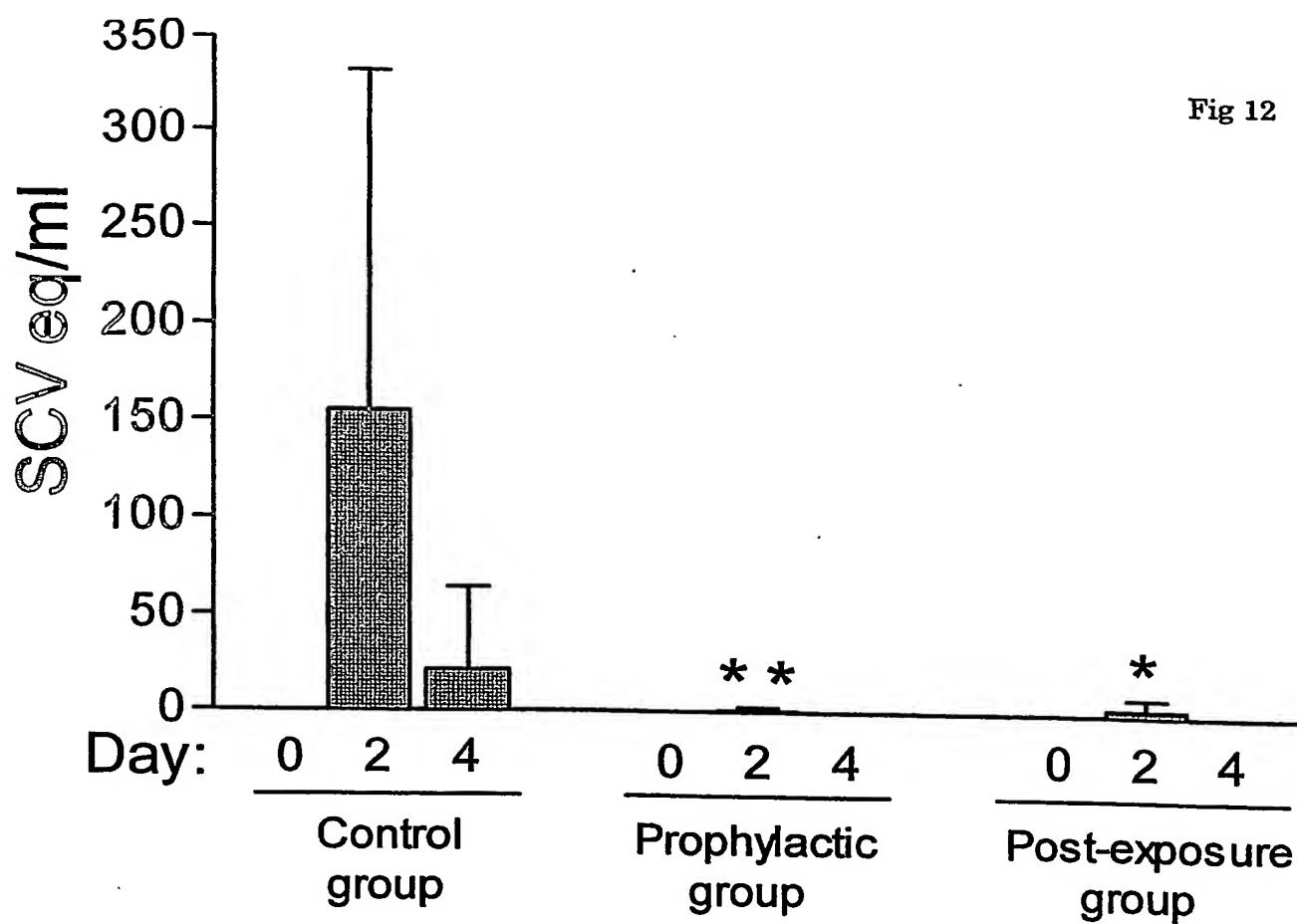


Fig 13

